

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/584,364  
Source: IFWP  
Date Processed by STIC: 07/07/2006

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 07/07/2006

PATENT APPLICATION: US/10/584,364

TIME: 14:48:54

Input Set : E:\10271-148-999.txt

Output Set: N:\CRF4\07072006\J584364.raw

3 <110> APPLICANT: Kinch, Michael S.  
 5 <120> TITLE OF INVENTION: EphA2 VACCINES  
 7 <130> FILE REFERENCE: 10271-148-999  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/584,364  
 C--> 9 <141> CURRENT FILING DATE: 2006-06-23  
 9 <150> PRIOR APPLICATION NUMBER: US 60/532,696  
 10 <151> PRIOR FILING DATE: 2003-12-24  
 12 <150> PRIOR APPLICATION NUMBER: US 60/602,588  
 13 <151> PRIOR FILING DATE: 2004-08-18  
 15 <150> PRIOR APPLICATION NUMBER: US 60/615,548  
 16 <151> PRIOR FILING DATE: 2004-10-01  
 18 <150> PRIOR APPLICATION NUMBER: US 60/617,564  
 19 <151> PRIOR FILING DATE: 2004-10-07  
 21 <160> NUMBER OF SEQ ID NOS: 72  
 23 <170> SOFTWARE: PatentIn version 3.2  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 3963  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Homo sapiens  
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 40 agagcgagaa gcgcggc atg gag ctc cag gca gcc cgc gcc tgc ttc gcc 170  
 41 Met Glu Leu Gln Ala Ala Arg Ala Cys Phe Ala  
 42 1 5 10  
 44 ctg ctg tgg ggc tgt gcg ctg gcc gcg gcc gcg gcg cag ggc aag 218  
 45 Leu Leu Trp Gly Cys Ala Leu Ala Ala Ala Ala Ala Gln Gly Lys  
 46 15 20 25  
 48 gaa gtg gta ctg ctg gac ttt gct gca gct gga ggg gag ctc ggc tgg 266  
 49 Glu Val Val Leu Leu Asp Phe Ala Ala Ala Gly Gly Glu Leu Gly Trp  
 50 30 35 40  
 52 ctc aca cac ccg tat ggc aaa ggg tgg gac ctg atg cag aac atc atg 314  
 53 Leu Thr His Pro Tyr Gly Lys Gly Trp Asp Leu Met Gln Asn Ile Met  
 54 45 50 55  
 56 aat gac atg ccg atc tac atg tac tcc gtg tgc aac gtg atg tct ggc 362  
 57 Asn Asp Met Pro Ile Tyr Met Tyr Ser Val Cys Asn Val Met Ser Gly  
 58 60 65 70 75  
 60 gac cag gac aac tgg ctc cgc acc aac tgg gtg tac cga gga gag gct 410  
 61 Asp Gln Asp Asn Trp Leu Arg Thr Asn Trp Val Tyr Arg Gly Glu Ala  
 62 80 85 90

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66				95					100					105			
68	ttc	cct	ggt	ggc	gcc	agc	tcc	tgc	aag	gag	act	ttc	aac	ctc	tac	tat	506
69	Phe	Pro	Gly	Gly	Ala	Ser	Ser	Cys	Lys	Glu	Thr	Phe	Asn	Leu	Tyr	Tyr	
70			110					115					120				
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73	Ala	Glu	Ser	Asp	Leu	Asp	Tyr	Gly	Thr	Asn	Phe	Gln	Lys	Arg	Leu	Phe	
74		125					130				135						
76	acc	aag	att	gac	acc	att	gcg	ccc	gat	gag	atc	acc	gtc	agc	agc	gac	602
77	Thr	Lys	Ile	Asp	Thr	Ile	Ala	Pro	Asp	Glu	Ile	Thr	Val	Ser	Ser	Asp	
78	140					145				150					155		
80	ttc	gag	gca	cgc	cac	gtg	aag	ctg	aac	gtg	gag	gag	cgc	tcc	gtg	ggg	650
81	Phe	Glu	Ala	Arg	His	Val	Lys	Leu	Asn	Val	Glu	Glu	Arg	Ser	Val	Gly	
82				160					165					170			
84	ccg	ctc	acc	cgc	aaa	ggc	ttc	tac	ctg	gcc	ttc	cag	gat	atc	ggt	gcc	698
85	Pro	Leu	Thr	Arg	Lys	Gly	Phe	Tyr	Leu	Ala	Phe	Gln	Asp	Ile	Gly	Ala	
86			175				180				185						
88	tgt	gtg	gcg	ctg	ctc	tcc	gtc	cgt	gtc	tac	tac	aag	aag	tgc	ccc	gag	746
89	Cys	Val	Ala	Leu	Leu	Ser	Val	Arg	Val	Tyr	Tyr	Lys	Lys	Cys	Pro	Glu	
90			190				195				200						
92	ctg	ctg	cag	ggc	ctg	gcc	cac	ttc	cct	gag	acc	atc	gcc	ggc	tct	gat	794
93	Leu	Leu	Gln	Gly	Leu	Ala	His	Phe	Pro	Glu	Thr	Ile	Ala	Gly	Ser	Asp	
94		205				210				215							
96	gca	cct	tcc	ctg	gcc	act	gtg	gcc	ggc	acc	tgt	gtg	gac	cat	gcc	gtg	842
97	Ala	Pro	Ser	Leu	Ala	Thr	Val	Ala	Gly	Thr	Cys	Val	Asp	His	Ala	Val	
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100	gtg	cca	ccg	ggg	ggt	gaa	gag	ccc	cgt	atg	cac	tgt	gca	gtg	gat	ggc	890
101	Val	Pro	Pro	Gly	Gly	Glu	Glu	Pro	Arg	Met	His	Cys	Ala	Val	Asp	Gly	
102				240					245				250				
104	gag	tgg	ctg	gtg	ccc	att	ggg	cag	tgc	ctg	tgc	cag	gca	ggc	tac	gag	938
105	Glu	Trp	Leu	Val	Pro	Ile	Gly	Gln	Cys	Leu	Cys	Gln	Ala	Gly	Tyr	Glu	
106			255				260				265						
108	aag	gtg	gag	gat	gcc	tgc	cag	gcc	tgc	tcg	cct	gga	ttt	ttt	aag	ttt	986
109	Lys	Val	Glu	Asp	Ala	Cys	Gln	Ala	Cys	Ser	Pro	Gly	Phe	Phe	Lys	Phe	
110		270				275					280						
112	gag	gca	tct	gag	agc	ccc	tgc	ttg	gag	tgc	cct	gag	cac	acg	ctg	cca	1034
113	Glu	Ala	Ser	Glu	Ser	Pro	Cys	Leu	Glu	Cys	Pro	Glu	His	Thr	Leu	Pro	
114		285				290				295							
116	tcc	cct	gag	ggt	gcc	acc	tcc	tgc	gag	tgt	gag	gaa	ggc	ttc	ttc	cgg	1082
117	Ser	Pro	Glu	Gly	Ala	Thr	Ser	Cys	Glu	Cys	Glu	Glu	Gly	Phe	Phe	Arg	
118	300				305				310					315			
120	gca	cct	cag	gac	cca	gcg	tcg	atg	cct	tgc	aca	cga	ccc	ccc	tcc	gcc	1130
121	Ala	Pro	Gln	Asp	Pro	Ala	Ser	Met	Pro	Cys	Thr	Arg	Pro	Pro	Ser	Ala	
122				320					325				330				
124	cca	cac	tac	ctc	aca	gcc	gtg	ggc	atg	ggt	gcc	aag	gtg	gag	ctg	cgc	1178
125	Pro	His	Tyr	Leu	Thr	Ala	Val	Gly	Met	Gly	Ala	Lys	Val	Glu	Leu	Arg	
126			335				340				345						
128	tgg	acg	ccc	cct	cag	gac	agc	ggg	ggc	cgc	gag	gac	att	gtc	tac	agc	1226

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133	Val	Thr	Cys	Glu	Gln	Cys	Trp	Pro	Glu	Ser	Gly	Glu	Cys	Gly	Pro	Cys	
134			365					370					375				
136	gag	gcc	agt	gtg	cgc	tac	tgc	gag	cct	cct	cac	gga	ctg	acc	cgc	acc	1322
137	Glu	Ala	Ser	Val	Arg	Tyr	Ser	Glu	Pro	Pro	His	Gly	Leu	Thr	Arg	Thr	
138	380						385					390				395	
140	agt	gtg	aca	gtg	agc	gac	ctg	gag	ccc	cac	atg	aac	tac	acc	ttc	acc	1370
141	Ser	Val	Thr	Val	Ser	Asp	Leu	Glu	Pro	His	Met	Asn	Tyr	Thr	Phe	Thr	
142					400					405					410		
144	gtg	gag	gcc	cgc	aat	ggc	gtc	tca	ggc	ctg	gta	acc	agc	cgc	agc	ttc	1418
145	Val	Glu	Ala	Arg	Asn	Gly	Val	Ser	Gly	Leu	Val	Thr	Ser	Arg	Ser	Phe	
146				415					420					425			
148	cgt	act	gcc	agt	gtc	agc	atc	aac	cag	aca	gag	ccc	ccc	aag	gtg	agg	1466
149	Arg	Thr	Ala	Ser	Val	Ser	Ile	Asn	Gln	Thr	Glu	Pro	Pro	Lys	Val	Arg	
150			430					435					440				
152	ctg	gag	ggc	cgc	agc	acc	acc	tgc	ctt	agc	gtc	tcc	tgg	agc	atc	ccc	1514
153	Leu	Glu	Gly	Arg	Ser	Thr	Thr	Ser	Leu	Ser	Val	Ser	Trp	Ser	Ile	Pro	
154		445					450					455					
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157	Pro	Pro	Gln	Gln	Ser	Arg	Val	Trp	Lys	Tyr	Glu	Val	Thr	Tyr	Arg	Lys	
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160	aag	gga	gac	tcc	aac	agc	tac	aat	gtg	cgc	cgc	acc	gag	ggt	ttc	tcc	1610
161	Lys	Gly	Asp	Ser	Asn	Ser	Tyr	Asn	Val	Arg	Arg	Thr	Glu	Gly	Phe	Ser	
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164	gtg	acc	ctg	gac	gac	ctg	gcc	cca	gac	acc	acc	tac	ctg	gtc	cag	gtg	1658
165	Val	Thr	Leu	Asp	Asp	Leu	Ala	Pro	Asp	Thr	Thr	Tyr	Leu	Val	Gln	Val	
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169	Gln	Ala	Leu	Thr	Gln	Glu	Gly	Gln	Gly	Ala	Gly	Ser	Lys	Val	His	Glu	
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181	Phe	Phe	Ile	His	Arg	Arg	Arg	Lys	Asn	Gln	Arg	Ala	Arg	Gln	Ser	Pro	
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185	Glu	Asp	Val	Tyr	Phe	Ser	Lys	Ser	Glu	Gln	Leu	Lys	Pro	Leu	Lys	Thr	
186				575					580				585				
188	tac	gtg	gac	ccc	cac	aca	tat	gag	gac	ccc	aac	cag	gct	gtg	ttg	aag	1946
189	Tyr	Val	Asp	Pro	His	Thr	Tyr	Glu	Asp	Pro	Asn	Gln	Ala	Val	Leu	Lys	
190			590					595					600				
192	ttc	act	acc	gag	atc	cat	cca	tcc	tgt	gtc	act	cgg	cag	aag	gtg	atc	1994
193	Phe	Thr	Thr	Glu	Ile	His	Pro	Ser	Cys	Val	Thr	Arg	Gln	Lys	Val	Ile	

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200	tcg ggg aag aag gag gtg ccg gtg gcc atc aag acg ctg aaa gcc ggc	2090		
201	Ser Gly Lys Lys Glu Val Pro Val Ala Ile Lys Thr Leu Lys Ala Gly			
202	640 645 650			
204	tac aca gag aag cag cga gtg gac ttc ctc ggc gag gcc ggc atc atg	2138		
205	Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu Gly Glu Ala Gly Ile Met			
206	655 660 665			
208	ggc cag ttc agc cac cac aac atc atc cgc cta gag ggc gtc atc tcc	2186		
209	Gly Gln Phe Ser His His Asn Ile Ile Arg Leu Glu Gly Val Ile Ser			
210	670 675 680			
212	aaa tac aag ccc atg atg atc act gag tac atg gag aat ggg gcc	2234		
213	Lys Tyr Lys Pro Met Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ala			
214	685 690 695			
216	ctg gac aag ttc ctt cgg gag aag gat ggc gag ttc agc gtg ctg cag	2282		
217	Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly Glu Phe Ser Val Leu Gln			
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220	ctg gtg ggc atg ctg cgg ggc atc gca gct ggc atg aag tac ctg gcc	2330		
221	Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met Lys Tyr Leu Ala			
222	720 725 730			
224	aac atg aac tat gtg cac cgt gac ctg gct gcc cgc aac atc ctc gtc	2378		
225	Asn Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val			
226	735 740 745			
228	aac agc aac ctg gtc tgc aag gtg tct gac ttt ggc ctg tcc cgc gtg	2426		
229	Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val			
230	750 755 760			
232	ctg gag gac gac ccc gag gcc acc tac acc acc agt ggc ggc aag atc	2474		
233	Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr Thr Ser Gly Gly Lys Ile			
234	765 770 775			
236	ccc atc cgc tgg acc gcc ccg gag gcc att tcc tac cgg aag ttc acc	2522		
237	Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ser Tyr Arg Lys Phe Thr			
238	780 785 790 795			
240	tct gcc agc gac gtg tgg agc ttt ggc att gtc atg tgg gag gtg atg	2570		
241	Ser Ala Ser Asp Val Trp Ser Phe Gly Ile Val Met Trp Glu Val Met			
242	800 805 810			
244	acc tat ggc gag cgg ccc tac tgg gag ttg tcc aac cac gag gtg atg	2618		
245	Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu Ser Asn His Glu Val Met			
246	815 820 825			
248	aaa gcc atc aat gat ggc ttc cgg ctc ccc aca ccc atg gac tgc ccc	2666		
249	Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro Thr Pro Met Asp Cys Pro			
250	830 835 840			
252	tcc gcc atc tac cag ctc atg atg cag tgc tgg cag cag gag cgt gcc	2714		
253	Ser Ala Ile Tyr Gln Leu Met Met Gln Cys Trp Gln Gln Glu Arg Ala			
254	845 850 855			
256	cgc cgc ccc aag ttc gct gac atc gtc agc atc ctg gac aag ctc att	2762		
257	Arg Arg Pro Lys Phe Ala Asp Ile Val Ser Ile Leu Asp Lys Leu Ile			
258	860 865 870 875			

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261 Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala Asp Phe Asp Pro Arg Val
262          880          885          890
264 tct atc cgg ctc ccc agc acg agc ggc tcg gag ggg gtg ccc ttc cgc      2858
265 Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser Glu Gly Val Pro Phe Arg
266          895          900          905
268 acg gtg tcc gag tgg ctg gag tcc atc aag atg cag cag tat acg gag      2906
269 Thr Val Ser Glu Trp Leu Glu Ser Ile Lys Met Gln Gln Tyr Thr Glu
270          910          915          920
272 cac ttc atg gcg gcc ggc tac act gcc atc gag aag gtg gtg cag atg      2954
273 His Phe Met Ala Ala Gly Tyr Thr Ala Ile Glu Lys Val Val Gln Met
274          925          930          935
276 acc aac gac gac atc aag agg att ggg gtg cgg ctg ccc ggc cac cag      3002
277 Thr Asn Asp Asp Ile Lys Arg Ile Gly Val Arg Leu Pro Gly His Gln
278 940          945          950          955
280 aag cgc atc gcc tac agc ctg ctg gga ctc aag gac cag gtg aac act      3050
281 Lys Arg Ile Ala Tyr Ser Leu Leu Gly Leu Lys Asp Gln Val Asn Thr
282          960          965          970
284 gtg ggg atc ccc atc tga gcctcgacag ggcttgagc cccatcggcc      3098
285 Val Gly Ile Pro Ile
286          975
288 aagaatactt gaagaaacag agtggcctcc ctgctgtgcc atgctgggccc actgggggact      3158
290 ttattttattt ctagttctttt cctccccctg caacttccgc tgaggggtct cggatgacac      3218
292 cctggcctga actgaggaga tgaccaggga tgctgggctg ggccctcttt cctgcgaga      3278
294 cgcacacagc tgagcactta gcaggcaccg ccacgtccca gcatccctgg agcaggagcc      3338
296 ccgccacagc cttcggacag acatatagga tattcccaag ccgaccttcc ctccgccttc      3398
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304 actggccaaa cccttgcttt cctgggcctt tgcaagatgc ttggttgtgt tgagggtttt      3638
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308 gctgggggaca gaggggtgtca aacattcgtg agctggggac tcaggggacc gtgctgcagg      3758
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334 Asp Phe Ala Ala Ala Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr
335          35          40          45
338 Gly Lys Gly Trp Asp Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile
339          50          55          60

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:66; N Pos. 1

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:22; Line(s) 1200

Seq#:33; Line(s) 2376

VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:4000 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66 after pos.:0